

APPENDIX A

Appendix A shows a comparison of the amino acid sequences of the bifunctional LKR-SDH proteins from *Arabidopsis* and corn, SEQ ID NO:112 and 122, respectively. Amino acids conserved among both sequences are indicated with an asterisk (*) on the top row; dashes are used by the program to maximize alignment of the sequences. The LKR and SDH domains (boxed sequences) were identified by Epelbaum et al. (*Plant Mol. Biol.* 35:735-748 (1997)) and Tang et al. (*Plant Cell* 9:1305-1316 (1997)).

SEQ_ID: 112	MNSNGHEEEKKLGNVGVGILSETVNWKERRTPLTPSHCARLLHGG-KDRTGISRIVVQPS
SEQ_ID: 122	-----CARLLLGGGKNGPRVNRIIVQPS
SEQ_ID: 112	-----
SEQ_ID: 122	AKRIHHDALYEHVGCEISDDLSDCGLILGIKQPELEMILPERAYAFFSHTHKAQKENMPL
SEQ_ID: 112	TRRIHHDAQYEDAGCEISEDLSECGLIIGIKQPKLQMLSDRAYAFFSHTHKAQKENMPL
SEQ_ID: 122	-----
SEQ_ID: 112	LDKILSERVTLCDYELIVGDHGKRLLAGFKYAGRAGLVDLHGLGQRYLSLGYSTPFLSL
SEQ_ID: 122	LDKILEERVSLFDYELIVGDDGKRSLAFGKFAGRAGLIDFLHGLGQRYLSLGYSTPFLSL
LKR domain	
SEQ_ID: 112	GASYYMSSLAAAKAAVISVGEEIASQGLPLGICPLVFVFTGTGNVSLAQEIFKLLPHTF
SEQ_ID: 122	GQSHMYPSLAAAKAAVIVVAEEIATFGLPSGICPIVFVFTGVGNVSQGAQEIFKLLPHTF
SEQ_ID: 112	-----
SEQ_ID: 122	VEPSKLPELFVKDKGQISQNGISTKRVYQVYGCIIITSQDMVEHKDPSKSFKDADYYAHPEH
SEQ_ID: 112	VDAEKLPEIF-QARNLSKQSQSTKRVFQLYGCVVTSDIVSHKDPTRQFDKGDYYAHPEH
SEQ_ID: 112	-----
SEQ_ID: 122	YNPVFHEKISPYTSVLVNCMYWEKRFPCLLSTKQLQDLTKKGLPLVGICDITCDIGGSIE
SEQ_ID: 112	YTPVFHERIAPYASVIVNCMYWEKRFPPLLNMDQLQQLMETGCPLVGVCIDITCDIGGSIE
SEQ_ID: 112	-----
SEQ_ID: 122	FVNRATLIDSPFFRFNPNSSYYDDMDGDGVLCMAVDILPTEFAKEASQHFGDILSGFVG
SEQ_ID: 112	FINKSTSIERPFFRYDPSKNSYHDDMEGAGVVCLADILPTEFSKEASQHFGNILSRLVA
SEQ_ID: 112	-----
SEQ_ID: 122	SLASMTEISDLPAHLKRACISYRGELTSLYEYIPRMRKSNPPEAQDNIIANGVSSQRTFN
SEQ_ID: 112	SLASVKQPAELPSYLRRACIAHAGRLTPLYEYIPRMRNTMIDLAPAKTNPL---PDKKYS
SEQ_ID: 112	-----
SEQ_ID: 122	ILVSLSGHLFDKFLINEALDMIEAAGGSFHLAKCELQOSADAESYSELEVGAADDKRVLDQ
SEQ_ID: 112	TLVSLSGHLFDKFLINEALDIETAGGSFHLVRCEVGQSTDDMSYSELEVGAADDTATLDK
SEQ_ID: 112	-----
SEQ_ID: 122	IIDS LTR LANP NEDYI SPH REANKI SLKIG KVQQ-ENEI KEKPEM T KK SG VL ILG AGR VC
SEQ_ID: 112	IIDS LT SLANE HGG DH DAQ EIE-LALKIG KVNEYETDVTIDKG SPK---ILILG AGR VC
SEQ_ID: 112	-----
SEQ_ID: 122	RPAADFLASVRTISSQQWYKTYFGADSEEKTDVHVIVASLYLKDAETVEG ISD VEA VRL
SEQ_ID: 112	RPAAEFLASYPDICT-----YGVDDHDADQI HVIVASLYQKDAEETVDG IENTTATQI



APPENDIX A (Continued)

SDH domain

SEQ_ID_112 DVSDSESSLKYVSQDVVLSSL PASCHAVVAKTCIELKKHLVTASYVDDETSMLHEAKS
SEQ_ID_122 DVADIGSLSDLVSQEVVISL LPASFHAAIAGVCIELKKHMVTASYVDEMSNL SQAAKD

SEQ_ID_112 AGITILGEMGLDPGIDHMMAMKMINDAHIKKGKVKSFTSYCGGLPSPAAANNPLAYKFSW
SEQ_ID_122 AGVTILCEMGLDPGIDHLMMSMKMIDEAHARKGKIKAFTSYCGGLPSPAAANNPLAYKFSW

SEQ_ID_112 NPAGAIRAGQNPAKYKSNGDIHV DKGKNLYDSAARFRVPNLP AFALECFPNRDSL VYGEH
SEQ_ID_122 NPAGALRSGKNPavykFLGETIHV DGHNLYESAKRLRLRELP AFALEHLPNRNSLIYGD

SEQ_ID_112 YGIESEATTIFRGTLRYEGFSIMIMATLSKLGFFDSEANQVLSTGKRITFGALLSNILNK-
SEQ_ID_122 YG SKEASTIYRATXRYEGESEIMVTL SKTGFFDAANHPL QDTSRPTYKGFLDELI NNT

SEQ_ID_112 --DADNESEPLAG-EEEISKRIIKLG--HSKETAAKAAKTIVFLGFNEEREVPSLCKSV
SEQ_ID_122 STINTDLDIEASGGYDDDLIARLLKLGCCNKEIAVKTVKTIKFLGLHEETQI PKGCSSP

SEQ_ID_112 FDATCYLMEEKLAYSGNEQDMVLLHHEVEVFLESKRIEKHTATLLEFGDIKNGQTTAM
SEQ_ID_122 FDVICQRMEQRMAYGHNEQDMVLLHHEVEVEY PDGQPAEKHQATLLEFGKVENGRSTAM

SEQ_ID_112 AKTVGIPAAIGALV LIEDKIKTRGVLRPLEAEVYLPALDIQAYGIKLMEAK
SEQ_ID_122 ALTVGIPAAIGALLLKNKVQTKGVTRPLQPEIYVPALEI LLESSGIKLVEKVE